

#15
12/28/94

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of
Thomas R. Adams et al.

Serial No. 08/113,561

Filed: August 25, 1993

For: METHODS AND COMPOSITIONS
FOR THE PRODUCTION OF
STABLY TRANSFORMED,
FERTILE MONOCOT PLANTS
AND CELLS THEREOF

§ Group Art Unit: 1804
§ Examiner: G. Benzion
§ Atty. Dkt.: DEKM:055/PAR

CERTIFICATE OF MAILING	
37 C.F.R. 1.8	
I hereby certify that this correspondence is being deposited with the U.S. Postal Service as First Class Mail in an envelope addressed to: Commissioner of Patents and Trademarks, Washington, D.C. 20231, on the date below:	
December 8, 1994	_____ Date
_____ David L. Parker	

STATEMENT AS REQUIRED UNDER 37 C.F.R. § 1.825(a) and (b)
AND STATEMENT AS REQUIRED UNDER 37 C.F.R. § 1.821(g)

ATTN: BOX SEQUENCE
Honorable Commissioner of
Patents and Trademarks
Washington, D.C. 20231

Sir:

Submitted herewith is a substitute computer readable form
and a substitute paper copy of the sequence listing of those
sequences in the captioned patent application, wherein minor
errors have been corrected. The substitute computer readable
form of the sequence listing is the same as the substitute paper
copy of the sequence listing. The sequence information provided

in the Specification is also the same as the sequence listing of the enclosed substitute computer readable and paper forms of the sequence listing.

In accordance with 37 C.F.R. § 1.821(g), it is herewith represented that no new matter is included with this submission.

Respectfully submitted,

David L. Parker
Reg. No. 32,165

ARNOLD, WHITE & DURKEE
P. O. Box 4433
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(512) 320-7200

Date: December 8, 1994

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Adams, Thomas R. et al.
- (ii) TITLE OF INVENTION: Methods and Compositions for the Production of Stably Transformed, Fertile Monocot Plants and Cells Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: P.O. Box 4433
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) COUNTRY: USA
 - (F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/113,561
 - (B) FILING DATE: 25-AUG-1993
 - (C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/565,844
 - (B) FILING DATE: 09-AUG-1990
 - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Parker, David L.
 - (B) REGISTRATION NUMBER: 32,165
 - (C) REFERENCE/DOCKET NUMBER: DEKM:055/PAR
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 512/418-3000
 - (B) TELEFAX: 713/789-2679
 - (C) TELEX: 79-0924

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acid residues
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
Met Ala Thr Val Pro Glu Leu Asn Cys Glu Met Pro Pro Ser Asp

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGGATCCGT CGACATGGTA AGCTTAGCGG GCCCC

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCGTCGA CCATGGCGCT TCAAGCTTC

29

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCAGCTGGTA CCGCGAAGTT CGAAGGGCT

29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTAGACAACA AAGCAGCAAC CATGGCCAGC ATGCAAGGCC TCATGCATC

49

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTGCTG

49

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acid residues
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ser Met Gln Gly Leu Met His Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acid residues
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Lys Cys Met Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGUGAAGUG AAGUGAAG

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1845 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC Me Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	48
1 5 10 15	
AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	96
20 25 30	
TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	144
35 40 45	
GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	192
50 55 60	
TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	240
65 70 75 80	
GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	288
85 90 95	
ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	336
100 105 110	
TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	384
115 120 125	
GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala	432
130 135 140	
ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val	480
145 150 155 160	
TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser	528
165 170 175	
GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg	576
180 185 190	
TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val	624
195 200 205	
CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg	672
210 215 220	

GAT	TGG	GTG	AGG	TAC	AAT	CAA	TTT	CGC	CGC	GAA	CTG	ACC	CTG	ACC	GTG	720
Asp	Trp	Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	
225		230						235							240	
CTC	GAT	ATC	GTG	GCT	CTG	TTC	CCA	AAT	TAC	GAT	AGC	CGC	CGC	TAC	CCA	768
Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Arg	Tyr	Pro	
	245							250							255	
ATT	CGA	ACC	GTG	TCC	CAA	CTG	ACC	CGC	GAA	ATT	TAC	ACC	AAC	CCA	GTG	816
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	
	260						265							270		
CTG	GAA	AAT	TTT	GAT	GGT	AGC	TTT	CGC	GGC	TCC	GCT	CAG	GGC	ATC	GAA	864
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	
	275						280							285		
CGC	AGC	ATT	AGG	AGC	CCA	CAT	CTG	ATG	GAT	ATC	CTG	AAC	AGC	ATC	ACC	912
Arg	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	
	290						295							300		
ATC	TAC	ACC	GAT	GCT	CAT	AGG	GGT	TAC	TAC	TAC	TGG	TCC	GGC	CAT	CAA	960
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Tyr	Tyr	Tyr	Tyr	Trp	Ser	Gly	His	Gln
	305						310							320		
ATC	ATG	GCT	TCC	CCT	G TG	GGC	TTT	TCC	GGG	CCA	GAA	TTC	ACC	TTT	CCA	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
	325						330							335		
CTG	TAC	GGC	ACG	ATG	GGC	AAT	GCC	GCT	CCA	CAA	CAA	CGC	ATT	GTG	GCT	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
	340						345							350		
CAA	CTG	GGT	CAG	GGC	GTG	TAC	CGC	ACC	CTG	TCC	TCC	ACC	CTG	TAC	CGC	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
	355						360							365		
CGC	CCT	TTT	AAT	ATC	GGC	ATC	AAC	AAC	CAG	CAA	CTG	TCC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
	370						375							380		
GGC	ACC	GAA	TTT	GCT	TAC	GGC	ACC	TCC	TCC	AAT	CTG	CCA	TCC	GCT	GTA	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
	385						390							400		
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAT	TCC	CTG	GAT	GAA	ATC	CCA	CCA	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
	405						410							415		
AAT	AAC	AAC	GTG	CCA	CCT	AGG	CAA	GGC	TTT	AGC	CAT	CGC	CTG	AGC	CAT	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
	420						425							430		
GTG	TCC	ATG	TTT	CGC	TCC	GGC	TTT	AGC	AAT	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
	435						440							445		
CGC	GCT	CCT	ATG	TTC	TCC	TGG	ATC	CAT	CGC	AGC	GCT	GAA	TTT	AAC	AAC	1392
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
	450						455							460		

ATC ATT GCC TCC GAT AGC ATT ACC CAA ATC CCT GCC GTG AAG GGC AAC Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn 465 470 475 480	1440
TTT CTG TTT AAT GGT TCC GTG ATT TCC GGC CCA GGC TTT ACC GGT GGC Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly 485 490 495	1488
GAC CTG GTG CGC CTG AAT AGC AGC GGC AAT AAC ATT CAG AAT CGC GGC Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly 500 505 510	1536
TAC ATT GAA GTG CCA ATT CAC TTC CCA TCC ACC TCC ACC CGC TAC CGC Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg 515 520 525	1584
GTG CGC GTG CGC TAC GCT TCC GTG ACC CCA ATT CAC CTC AAC GTT AAC Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn 530 535 540	1632
TGG GGC AAT TCC TCC ATT TTT TCC AAT ACC GTG CCA GCT ACC GCT ACC Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr 545 550 555 560	1680
TCC CTG GAT AAT CTG CAA TCC AGC GAT TTT GGT TAC TTT GAA AGC GCC Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala 565 570 575	1728
AAT GCT TTT ACC TCC TCC CTG GGT AAT ATC GTG GGT GTG CGC AAT TTT Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe 580 585 590	1776
AGC GGC ACC GCC GGC GTG ATC ATC GAC CGC TTT GAA TTT ATT CCA GTG Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val 595 600 605	1824
ACC GCC ACC CTC GAG TAGGTA Thr Ala Thr Leu Glu 610	1845

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 613 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser

35

40

45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
 50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
 100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
 115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
 130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
 145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
 165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
 180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
 195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
 210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
 225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
 245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
 260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
 275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
 290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
 305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
 325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
 340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg

355

360

365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
 370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
 385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
 405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
 420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
 435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
 450 455 460

Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
 465 470 475 480

Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
 485 490 495

Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
 500 505 510

Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
 515 520 525

Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
 530 535 540

Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
 545 550 555 560

Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
 565 570 575

Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
 580 585 590

Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
 595 600 605

Thr Ala Thr Leu Glu
 610

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1848 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1 5 10 15	
AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
20 25 30	
TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
35 40 45	
GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
50 55 60	
TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
65 70 75 80	
GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC	288
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
85 90 95	
ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA	336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	
100 105 110	
TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA	384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	
115 120 125	
GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT	432
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala	
130 135 140	
ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG	480
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val	
145 150 155 160	
TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC	528
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser	
165 170 175	
GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC	576
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg	
180 185 190	
TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG	624
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val	
195 200 205	
CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC	672

Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	
210						215				220						
GAT	TGG	GTG	AGG	TAC	AAT	CAA	TTT	CGC	CGC	GAA	CTG	ACC	CTG	ACC	GTG	720
Asp	Trp	Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	
225						230				235					240	
CTC	GAT	ATC	GTG	GCT	CTG	TTC	CCA	AAT	TAC	GAT	AGC	CGC	CGC	TAC	CCA	768
Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Arg	Tyr	Pro	
						245			250					255		
ATT	CGA	ACC	GTG	TCC	CAA	CTG	ACC	CGC	GAA	ATT	TAC	ACC	AAC	CCA	GTG	816
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	
						260			265					270		
CTG	GAA	AAT	TTT	GAT	GGT	AGC	TTT	CGC	GGC	TCC	GCT	CAG	GGC	ATC	GAA	864
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	
						275			280					285		
CGC	AGC	ATT	AGG	AGC	CCA	CAT	CTG	ATG	GAT	ATC	CTG	AAC	AGC	ATC	ACC	912
Arg	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	
						290			295					300		
ATC	TAC	ACC	GAT	GCT	CAT	AGG	GGT	TAC	TAC	TAC	TGG	TCC	GGC	CAT	CAA	960
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Tyr	Tyr	Tyr	Tyr	Trp	Ser	Gly	His	
						305			310					320		
ATC	ATG	GCT	TCC	CCT	GTG	GGC	TTT	TCC	GGG	CCA	GAA	TTC	ACC	TTT	CCA	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
						325			330					335		
CTG	TAC	GGC	ACG	ATG	GGC	AAT	GCC	GCT	CCA	CAA	CAA	CGC	ATT	GTG	GCT	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
						340			345					350		
CAA	CTG	GGT	CAG	GGC	GTG	TAC	CGC	ACC	CTG	TCC	TCC	ACC	CTG	TAC	CGC	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
						355			360					365		
CGC	CCT	TTT	AAT	ATC	GGC	ATC	AAC	AAC	CAG	CAA	CTG	TCC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
						370			375					380		
GGC	ACC	GAA	TTT	GCT	TAC	GGC	ACC	TCC	TCC	AAT	CTG	CCA	TCC	GCT	GTA	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
						385			390					400		
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAT	TCC	CTG	GAT	GAA	ATC	CCA	CCA	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
						405			410					415		
AAT	AAC	AAC	GTG	CCA	CCT	AGG	CAA	GGC	TTT	AGC	CAT	CGC	CTG	AGC	CAT	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
						420			425					430		
GTG	TCC	ATG	TTT	CGC	TCC	GGC	TTT	AGC	AAT	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
						435			440					445		
CGC	GCT	CCT	ATG	TTC	TCC	TGG	ATC	CAC	CGC	TCC	GCT	GAG	TTC	AAC	AAC	1392

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn			
450	455	460	
ATC ATC CCG TCC TCC CAA ATC ACC CAA ATC CCG CTC ACC AAG TCC ACG			1440
Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr			
465	470	475	480
AAC CTC GGC TCC GGC ACG TCC GTC GTC AAG GGC CCG GGC TTC ACC GGC			1488
Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly			
485	490	495	
GGC GAC ATC CTC CGC CGC ACG TCC CCG GGC CAG ATC TCC ACC CTC CGC			1536
Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg			
500	505	510	
GTC AAC ATC ACG GCT CCG CTG AGC CAG CGC TAC AGG GTG CGC ATC AGA			1584
Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg			
515	520	525	
TAC GCT AGC ACG ACC AAC CTG CAA TTC CAC ACG TCC ATC GAC GGC AGA			1632
Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg			
530	535	540	
CCG ATC AAC CAG GGC AAC TTC AGC GCG ACG ATG AGC TCC GGG TCC AAC			1680
Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn			
545	550	555	560
CTC CAG TCC GGC TCC TTC CGC ACG GTC GGT TTC ACC ACG CCG TTC AAC			1728
Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn			
565	570	575	
TTC TCC AAC GGC TCC TCC GTC TTC ACG CTC TCC GCT CAC GTC TTC AAC			1776
Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn			
580	585	590	
TCC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTC CCG GCC GAG			1824
Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu			
595	600	605	
GTC ACC TTC GAG CTC GAG TAGGTA			1848
Val Thr Phe Glu Leu Glu			
610			

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu			
1	5	10	15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly			
20	25	30	

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
 355 360 365
 Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
 370 375 380
 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
 385 390 395 400
 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
 405 410 415
 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
 420 425 430
 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
 435 440 445
 Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
 450 455 460
 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
 465 470 475 480
 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
 485 490 495
 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
 500 505 510
 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
 515 520 525
 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
 530 535 540
 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
 545 550 555 560
 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
 565 570 575
 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
 580 585 590
 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
 595 600 605
 Val Thr Phe Glu Leu Glu
 610

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ile Thr Phe Thr Gly
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTGGCAGC CATCACGTTCA CGGGAAAGTA TTGTC

35

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTGGCAGC AGAAAAACAA GTAGTTGAGA ACTAAGAAGA AGAAA

45

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATCGAGACA AGCACGGTCA ACTTC

25

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGTCCCTGG AGGCACAGGG CTTCAAGA

28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCTTGCAGC GAGTACATAC ATACTAGGCA GCCAGGCAGC CATGGCGCCC ACCGTGATGA	60
TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGCT CAAGTCCACC GCCAGCCTCC	120
CCGTCGCCCCG CCGGTCCCTCC AGAACGCCTCG GCAACGTCAG CAACGGCGGA AGGATCCGGT	180
GCATG	185

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACGTCGCTCA TGTATGTATG ATCCGTCGGT CCGTCGGTAC CGCGGGTGGC ACTACTACCG	60
GAGCAGCCGG TGGCGGCAGC GAGGCAAGGT CCCCGAGTTC AGGTGGCGGT CGGAGGGGCA	120
GCGGGCGGCC AGGAGGTCTT CGGAGCCGTT GCAGTCGTTG CCGCCTTCCT AGGCCAC	177

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATCACTTTCA CGGGA	15
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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCACGTTCA CGGCA	15
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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTTACCTAC TAATTGTTCT TGG

23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGGTACAT ATTTGCCTTG GG

22

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AACCCTGAAT GGAAGTGC

18

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACGGACAGAT GCAGATTGG

19